



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/674,237B

DATE: 07/26/2004

TIME: 15:38:46

Input Set : A:\3477.89.ST25.txt

Output Set: N:\CRF4\07262004\I674237B.raw

3 <110> APPLICANT: Egan, Sean E.
 4 Wang, Wei
 5 Sengar, Ameet
 7 <120> TITLE OF INVENTION: ESE GENES AND PROTEINS
 9 <130> FILE REFERENCE: 3477.89
 11 <140> CURRENT APPLICATION NUMBER: US 09/674,237B
 C--> 12 <141> CURRENT FILING DATE: 2001-07-24
 14 <150> PRIOR APPLICATION NUMBER: PCT/CA99/00375
 15 <151> PRIOR FILING DATE: 1999-04-27
 17 <150> PRIOR APPLICATION NUMBER: US 60/118,739
 18 <151> PRIOR FILING DATE: 1999-02-05
 20 <150> PRIOR APPLICATION NUMBER: CA 2230201
 21 <151> PRIOR FILING DATE: 1998-04-27
 23 <160> NUMBER OF SEQ ID NOS: 35
 25 <170> SOFTWARE: PatentIn version 3.2
 27 <210> SEQ ID NO: 1
 28 <211> LENGTH: 5084
 29 <212> TYPE: DNA
 30 <213> ORGANISM: Mus musculus
 32 <400> SEQUENCE: 1

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37	cgggcgaaa tggtgtgcgc ggctcgaaa tcggcgatcc tcgcgcggcg	tgccggctgc	180
39	actgatttgt gtgaggcg gcccggcgc cccgcggaaa gatgaggcg	cgatcagcaa	240
41	gttgaacgta atagaaccat ggctcgttt cccacaccc tcgggtgttag	cctggatgtc	300
43	tggccataa ctgtggagga aaggggcaag catgaccaggc agttcccttag	cctgaagccg	360
45	atagcggtat ttattactgg tcatcaagcg aggaactttt tttccaaatc	tgggttacct	420
47	caggctgtct tagcacaat atggcgcta gcccggatcataacgatgg	aaggatggat	480
49	caagtggaaat ttccatagc catgaagctt atcaaactga agctacaagg	atatcagctc	540
51	ccctccacac ttccccctgt catgaaacag caaccaggatccatccat	tgcaccagca	600
53	tgggtatag gaggattgc tagcatgcca ccactcacag ctgttgc	tgtgccaatg	660
55	ggccatccattc cagttgttgg aatgtctcca cccttagat cttctgtccc	tccaggcagca	720
57	gtgcctcccc tggctaaacgg ggctccccc gtcatacaggc ctctgcgtc	gtttgcgtat	780
59	cctgcaggcca catggccaaa gagttctcc ttcaggcaggat ctggccagg	gtcacaattaa	840
61	aacactaagt tacagaaggc acaatcatc gatgtcgcca gcccctcc	agcagcagaa	900
63	tggctgtgc ctcagtcatac aaggctgaaa tacaggcagt tattcaacag	ccacgacaaa	960
65	actatgatg gacactaac agtccccag gcaagaacta ttctcatgca	atcaagtta	1020
67	ccccaggctc agctggcttc aatatggaaat cttctgaca ttgatcaaga	tggaaaactc	1080
69	actgcagaag aatttacatc agctatgcac ctaattgtat ttgccatgtc	tggtcagccaa	1140
71	ctggcgcccg tcctgcctcc agaatacatc cctccttc tcaagaagagt	tgcgtccggc	1200
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P. b

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83	cagcgggagc	tggagcggca	gcgagaggag	gagaggagga	aggagatcga	gaggcgcgag	1560
85	gccgc当地	gggaactgga	aaggcagcg	caacttgaat	gggaacggaa	ccggagacag	1620
87	gaactcctga	atcagaggaa	caaggagcg	gagggcaccg	tggcctgaa	ggcaaggagg	1680
89	aagactctgg	agtttgagtt	agaagctctg	aatgacaaaaa	agcatcagct	agaaggaaaa	1740
91	cttcaggata	tcagggtgtcg	actggcaacc	cagaggcaag	aaatttgagag	cacgaacaag	1800
93	tcttagagago	taagaattgc	tgaaatcacc	cacttacagc	agcagttgca	ggaatctcag	1860
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99	gagctggccc	ggcagcagct	ccgggagcg	ctggacgagg	tggagagaga	gaccaggta	2040
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125	gagccctcoa	caaccccc当地	caactggca	gacttcagtt	ccacgtgccc	cagcagctca	2820
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169	gttgcata	atcgaaatgt	ctgactact	gcgtgcagag	gcagaagcaa	attgcagaac	4140
171	tgcacagggt	ggtggcctt	tttggggctt	tccttagtac	tcagactgac	cgccccccg	4200
173	ttcacacagg	cgcttcaat	agttttaaga	ttattttaa	atgtgtat	tagccat	4260
175	ataaaaaatct	caatcaatta	cttcttgc	tatgggtt	ttacaaaaac	acccactatc	4320

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 195 ggaatatctt gaacaagtaa tcttcttgac aagaaagaat gtatagaagt ctccctgcaa 4920
 197 ttaatttccc agtgttaca ttttttaact agactgtggg ggttgcata gattaatatg 4980
 199 aaatggcgct cctggccgt gtgtgtgtt aacttgtctg tagctgaagc cgtgtgtcct 5040
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 218 1 5 10 15
 220 ata act gtg gag gaa agg gcc aag cat gac cag cag ttc ctt agc ctg 96
 221 Ile Thr Val Glu Glu Arg Ala Lys His Asp Gln Gln Phe Leu Ser Leu
 222 20 25 30
 224 aag ccg ata gcg gga ttt att act ggt gat caa gcg agg aac ttt ttt 144
 225 Lys Pro Ile Ala Gly Phe Ile Thr Gly Asp Gln Ala Arg Asn Phe Phe
 226 35 40 45
 228 ttc caa tct ggg tta cct cag cct gtc tta gca caa ata tgg gcg cta 192
 229 Phe Gln Ser Gly Leu Pro Gln Pro Val Leu Ala Gln Ile Trp Ala Leu
 230 50 55 60
 232 gcg gac atg aat aac gat gga agg atg gat caa gtg gaa ttt tcc ata 240
 233 Ala Asp Met Asn Asn Asp Gly Arg Met Asp Gln Val Glu Phe Ser Ile
 234 65 70 75 80
 236 gcc atg aag ctt atc aaa ctg aag cta caa gga tat cag ctc ccc tcc 288
 237 Ala Met Lys Leu Ile Lys Leu Lys Leu Gln Gly Tyr Gln Leu Pro Ser
 238 85 90 95
 240 aca ctt ccc cct gtc atg aaa cag caa cca gtg gct att tcc agt gca 336
 241 Thr Leu Pro Pro Val Met Lys Gln Gln Pro Val Ala Ile Ser Ser Ala
 242 100 105 110
 244 cca gca ttt ggt ata gga ggg att gct agc atg cca cca ctc aca gct 384
 245 Pro Ala Phe Gly Ile Gly Gly Ile Ala Ser Met Pro Pro Leu Thr Ala
 246 115 120 125
 248 gtt gct cct gtg cca atg ggc tcc att cca gtt gtt gga atg tct cca 432
 249 Val Ala Pro Val Pro Met Gly Ser Ile Pro Val Val Gly Met Ser Pro
 250 130 135 140

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256	ggg gct cct ccc gtc ata cag cct ctg cct gcg ttt gcg cat cct gca	528
257	Gly Ala Pro Pro Val Ile Gln Pro Leu Pro Ala Phe Ala His Pro Ala	
258	165 170 175	
260	gcc aca tgg cca aag agt tct tcc ttc agc aga tct ggt cca ggg tca	576
261	Ala Thr Trp Pro Lys Ser Ser Ser Phe Ser Arg Ser Gly Pro Gly Ser	
262	180 185 190	
264	caa tta aac act aag tta cag aag gca caa tca ttc gat gtc gcc agc	624
265	Gln Leu Asn Thr Lys Leu Gln Lys Ala Gln Ser Phe Asp Val Ala Ser	
266	195 200 205	
268	gcc cct cca gca gca gaa tgg gct gtg cct cag tca tca agg ctg aaa	672
269	Ala Pro Pro Ala Ala Glu Trp Ala Val Pro Gln Ser Ser Arg Leu Lys	
270	210 215 220	
272	tac agg cag tta ttc aac agc cac gac aaa act atg agt gga cac tta	720
273	Tyr Arg Gln Leu Phe Asn Ser His Asp Lys Thr Met Ser Gly His Leu	
274	225 230 235 240	
276	aca ggt ccc cag gca aga act att ctc atg caa tca agt tta ccc cag	768
277	Thr Gly Pro Gln Ala Arg Thr Ile Leu Met Gln Ser Ser Leu Pro Gln	
278	245 250 255	
280	gct cag ctg gct tca ata tgg aat ctt tct gac att gat caa gat gga	816
281	Ala Gln Leu Ala Ser Ile Trp Asn Leu Ser Asp Ile Asp Gln Asp Gly	
282	260 265 270	
284	aaa ctc act gca gaa gaa ttt atc cta gct atg cac cta att gat gtt	864
285	Lys Leu Thr Ala Glu Glu Phe Ile Leu Ala Met His Leu Ile Asp Val	
286	275 280 285	
288	gcc atg tct ggt cag cca ctg ccg ccc gtc ctg cct cca gaa tac atc	912
289	Ala Met Ser Gly Gln Pro Leu Pro Pro Val Leu Pro Pro Glu Tyr Ile	
290	290 295 300	
292	cct cct tcc ttc aga aga gtt cgc tcc ggc agt ggg atg tcc gtc ata	960
293	Pro Pro Ser Phe Arg Arg Val Arg Ser Gly Ser Gly Met Ser Val Ile	
294	305 310 315 320	
296	agc tct tct gtg gat cag agg ctg cct gag gag ccg tcg tca gag	1008
297	Ser Ser Ser Val Asp Gln Arg Leu Pro Glu Glu Pro Ser Ser Glu	
298	325 330 335	
300	gat gag cag cag cca gag aag aaa ctg cct gtg aca ttt gaa gat aag	1056
301	Asp Glu Gln Gln Pro Glu Lys Lys Leu Pro Val Thr Phe Glu Asp Lys	
302	340 345 350	
304	aag cgg gag aac ttc gag cga ggc agt gtg gag ctg gag aag cgc cgc	1104
305	Lys Arg Glu Asn Phe Glu Arg Gly Ser Val Glu Leu Glu Lys Arg Arg	
306	355 360 365	
308	caa gcg ctc ttg gag cag cag cgc aaa gag cag gag cgg ttg gct cag	1152
309	Gln Ala Leu Leu Glu Gln Gln Arg Lys Glu Gln Glu Arg Leu Ala Gln	
310	370 375 380	
312	ctg gag cgc gcc gag cag gag agg aaa gag cgg gag cgc cag gag cag	1200
313	Leu Glu Arg Ala Glu Gln Glu Arg Lys Glu Arg Glu Arg Gln Glu Gln	
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321	Glu	Leu	Glu	Arg	Gln	Arg	Glu	Glu	Arg	Arg	Lys	Glu	Ile	Glu	Arg			
322					420				425					430				
324	cgc	gag	gcc	gca	aaa	cg	gaa	ctg	gaa	agg	cag	cga	caa	ctt	gaa	tgg	1344	
325	Arg	Glu	Ala	Ala	Lys	Arg	Glu	Leu	Glu	Arg	Gln	Arg	Gln	Leu	Glu	Trp		
326					435				440					445				
328	gaa	cg	aa	cg	ag	ca	g	ctc	ctg	aat	cag	agg	aac	aag	gag	cag	1392	
329	Glu	Arg	Asn	Arg	Arg	Gln	Glu	Leu	Leu	Asn	Gln	Arg	Asn	Lys	Glu	Gln		
330					450				455					460				
332	gag	ggc	acc	gt	gt	ct	ct	aag	gca	agg	agg	act	ctg	gag	ttt	gag	1440	
333	Glu	Gly	Thr	Val	Val	Leu	Lys	Ala	Arg	Arg	Lys	Thr	Leu	Glu	Phe	Glu		
334	465				470				475						480			
336	tta	gaa	gct	ct	ct	aat	gac	aaa	aag	cat	cag	cta	gaa	gga	aaa	ctt	cag	1488
337	Leu	Glu	Ala	Leu	Asn	Asp	Lys	Lys	His	Gln	Leu	Glu	Gly	Lys	Leu	Gln		
338					485				490						495			
340	gat	atc	agg	tgt	cg	ct	gca	acc	cag	agg	caa	gaa	att	gag	agc	acg	1536	
341	Asp	Ile	Arg	Cys	Arg	Leu	Ala	Thr	Gln	Arg	Gln	Glu	Ile	Glu	Ser	Thr		
342					500				505						510			
344	aac	aag	tct	aga	gag	ct	aga	att	gct	gaa	atc	acc	cac	tta	cag	cag	1584	
345	Asn	Lys	Ser	Arg	Glu	Leu	Arg	Ile	Ala	Glu	Ile	Thr	His	Leu	Gln	Gln		
346					515				520						525			
348	cag	ttg	cag	gaa	tct	cg	caa	atg	ctt	gga	aga	ctt	att	cca	gag	aaa	1632	
349	Gln	Leu	Gln	Glu	Ser	Gln	Gln	Met	Leu	Gly	Arg	Leu	Ile	Pro	Glu	Lys		
350					530				535						540			
352	cag	ata	ctc	agt	gac	cg	tg	aaa	caa	gtc	cag	cag	aac	agt	ttg	cat	1680	
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356	aga	gac	tcg	ctt	acc	ctc	aaa	aga	gcc	ttg	gaa	gca	aag	gag	ctg	1728		
357	Arg	Asp	Ser	Leu	Leu	Thr	Leu	Lys	Arg	Ala	Leu	Glu	Ala	Lys	Glu	Leu		
358					565				570						575			
360	gcc	cg	cag	ctc	cg	gag	cg	ct	gac	gag	gtg	gag	aga	gag	acc	1776		
361	Ala	Arg	Gln	Gln	Leu	Arg	Glu	Gln	Leu	Asp	Glu	Val	Glu	Arg	Glu	Thr		
362					580				585						590			
364	agg	tca	aag	ctg	cag	gag	att	gat	gtt	ttc	aac	aac	cag	ctg	aag	gaa	1824	
365	Arg	Ser	Lys	Leu	Gln	Glu	Ile	Asp	Val	Phe	Asn	Asn	Gln	Leu	Lys	Glu		
366					595				600						605			
368	ctg	aga	gag	ata	cat	agc	aaa	cag	caa	ctc	cag	aag	agg	tcc	ctg		1872	
369	Leu	Arg	Glu	Ile	His	Ser	Lys	Gln	Gln	Leu	Gln	Lys	Gln	Arg	Ser	Leu		
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373	Glu	Ala	Ala	Arg	Leu	Lys	Gln	Lys	Glu	Gln	Arg	Lys	Ser	Leu	Glu			
374	625				630				635						640			
376	tta	gag	aag	caa	aag	gaa	gac	gct	cag	aga	cga	gtt	cag	gaa	agg	gac	1968	
377	Leu	Glu	Lys	Gln	Lys	Glu	Asp	Ala	Gln	Arg	Arg	Val	Gln	Glu	Arg	Asp		
378					645				650						655			
380	aag	caa	tgg	ctg	gag	cat	gtg	cag	cag	gag	gag	cag	cca	cgc	ccc	cg	2016	
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:18; N Pos. 102,103

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:2218 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:60